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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/905,743

DATE: 11/21/2001
TIME: 12:13:21

Input Set : N:\Crf3\RULE60\09905743.txt
Output Set: N:\CRF3\11212001\I905743.raw

3 <110> APPLICANT: Chadwick, Brian Paul
 4 Frischauf, Anna-Maria
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
 7 POLYPEPTIDES AND NUCLEIC ACIDS
 9 <130> FILE REFERENCE: 9598-066
 11 <140> CURRENT APPLICATION NUMBER: 09/905,743
 12 <141> CURRENT FILING DATE: 2001-07-13
 14 <150> PRIOR APPLICATION NUMBER: 09/240,639
 15 <151> PRIOR FILING DATE: 1999-01-29
 17 <160> NUMBER OF SEQ ID NOS: 29
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 2762
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (232)..(1599)
 30 <400> SEQUENCE: 1
 31 gtggggtcgt atcccgccgg tggaggccgg ggtggcggc gcccggggccgg gggagcccaa 60
 33 aagaccggct gccgcctgct ccccgaaaaa gggcactcggt ctccgtgggt gtggcggagc 120
 35 gcgcggtgca tggaatgggc tatgtgaatg aaaaaaggtt tccgttatga aacttccaga 180
 37 aaaacgagct acattttca gcagccgcag cacggtcctt ggcaaacaag g atg aga 237
 38 Met Arg
 39 1
 41 aaa ata tcc aac cac ggg agc ctg cggt gtg gca tac ccc 285
 42 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
 43 5 10 15
 45 ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg 333
 46 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
 47 20 25 30
 49 cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc 381
 50 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
 51 35 40 45 50
 53 ccg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct 429
 54 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
 55 55 60 65
 57 gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc 477
 58 Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
 59 70 75 80
 61 act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa 525
 62 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
 63 85 90 95
 65 act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt 573
 66 Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
 67 100 105 110
 69 tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa 621

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70	Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu			
71	115	120	125	130
73	cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc	669		
74	Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala			
75	135	140	145	
77	acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga	717		
78	Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly			
79	150	155	160	
81	gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca	765		
82	Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala			
83	165	170	175	
85	tgc cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca	813		
86	Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr			
87	180	185	190	
89	gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc	861		
90	Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser			
91	195	200	205	210
93	ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga	909		
94	Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly			
95	215	220	225	
97	gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag	957		
98	Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln			
99	230	235	240	
101	gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc	1005		
102	Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr			
103	245	250	255	
105	tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca	1053		
106	Tyr Lys Leu Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala			
107	260	265	270	
109	cgc ctg gcg atc ctg ggc gtg gag ggg cag cct gct aag gat gga	1101		
110	Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly			
111	275	280	285	290
113	aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg	1149		
114	Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp			
115	295	300	305	
117	gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca	1197		
118	Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala			
119	310	315	320	
121	agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac	1245		
122	Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn			
123	325	330	335	
125	aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc	1293		
126	Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe			
127	340	345	350	
129	tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag	1341		
130	Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu			
131	355	360	365	370
133	aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac	1389		
134	Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr			

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135	375	380	385	
137	gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc			1437
138	Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys			
139	390	395	400	
141	atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc			1485
142	Met Asp Leu Thr Tyr Val Ser Leu Leu Gln Glu Phe Gly Phe Pro			
143	405	410	415	
145	agg agc aaa gtg ctg aag ctc act cg ^g aaa att gac aat gtt gag acc			1533
146	Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr			
147	420	425	430	
149	agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga			1581
150	Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg			
151	435	440	445	450
153	cag aag agt cca gcc tca tagtggccga gccatccc ^t tccccgtcag			1629
154	Gln Lys Ser Pro Ala Ser			
155	455			
157	cagtgtctgt gtgtctgcat aaaccctcct gtcctggacg tgacttcatc ctgaggagcc			1689
159	acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca gaaggcctgg			1749
161	tgctgccctg gcatcagcct cttccagtc ^a catctggcca gagggctgtc tggacctggg			1809
163	ccctgctcaa tgccacactgt ctgcctggc tccaagtggg caggaccagg acagaaccac			1869
165	aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catccccatg ccccg ^t ccgc			1929
167	ggggctgtgg ctgctgtgt gcatgtccct gc ^g atggag tcttgc ^t tcc cagcctgtca			1989
169	gtttcctccc cagggcagag ctccccttcc tgcaagagtc tggaggccg tgcaaggctgt			2049
171	cctggctgct ctggggaa ^g cg ^g aggacag ccataaacacc cccgggacag taggtctggg			2109
173	cggc ^g accact gggaa ^{ct} ctg gacttgatg tg ^t ttgc ^t tct tccttggta tgaatgtgtg			2169
175	agttcaccca gaggc ^t ctgctgc ^t ctc ^t ccacac attgtgtgg ttggggtaa t ^t gatggaggg			2229
177	agacacactot tcatagac ^g g cagg ^t gcccc ccttc ^t cagg agtctcc ^t ccag catgggc ^t gga			2289
179	tgccgggcat gagctgtgt aaactattt ^g tggctgtgt gcttg ^t gatgta cgtctctgtc			2349
181	gtgtgggtgc caagtgttt ^t g t ^t tagaaact gtgttctgag cccccc ^t ttt ^t cc tggacaccaa			2409
183	ctgtgtctgt tgaatgtatc gta ^t ctgtga gctttcccc cctagccagg gccatgtctt			2469
185	aggtgcagct gtgccacggg tca ^t gctgagc cacatccca gaaccaagct ctgg ^t gtct			2529
187	cgggcccacca tccgccccacc tcgggctgac cccaccc ^t tct ccatggacag t ^t tgagcccc			2589
189	ggggcgtgca tcc ^t gctc ^t g t ^t g ^t ggcgtca gtgtcggg ^t gc tgagcccc ^t gagctgctt ^t c			2649
191	agtgaatgt ^t a cagtggccgg cacgagctga acctcatgt ^t g ttccactccc aataaaaggt			2709
193	tgacaggggc ttctc ^t ttca aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaa			2762
196	<210> SEQ ID NO: 2			
197	<211> LENGTH: 456			
198	<212> TYPE: PRT			
199	<213> ORGANISM: Homo sapiens			
201	<400> SEQUENCE: 2			
202	Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala			
203	1 5 10 15			
205	Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile			
206	20 25 30			
208	Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg			
209	35 40 45			
211	Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly			
212	50 55 60			
214	Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala			

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215	65	70	75	80
217	Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro			
218	85	90	95	
220	Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro			
221	100	105	110	
223	Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile			
224	115	120	125	
226	Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp			
227	130	135	140	
229	Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu			
230	145	150	155	160
232	Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe			
233	165	170	175	
235	Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn			
236	180	185	190	
238	Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr			
239	195	200	205	
241	Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu			
242	210	215	220	
244	Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr			
245	225	230	235	240
247	Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn			
248	245	250	255	
250	Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met			
251	260	265	270	
253	Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys			
254	275	280	285	
256	Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly			
257	290	295	300	
259	Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala			
260	305	310	315	320
262	Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu			
263	325	330	335	
265	Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr			
266	340	345	350	
268	Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp			
269	355	360	365	
271	Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala			
272	370	375	380	
274	Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe			
275	385	390	395	400
277	Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Gln Glu Phe Gly			
278	405	410	415	
280	Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val			
281	420	425	430	
283	Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu			
284	435	440	445	
286	Asn Arg Gln Lys Ser Pro Ala Ser			
287	450	455		

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290 <210> SEQ ID NO: 3
 291 <211> LENGTH: 2797
 292 <212> TYPE: DNA
 293 <213> ORGANISM: Homo sapiens
 295 <220> FEATURE:
 296 <221> NAME/KEY: CDS
 297 <222> LOCATION: (83)..(1669)
 299 <400> SEQUENCE: 3
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 302 ctccgcacag ctaggagaaa ag atg ttc act gtg ctg acc cgc caa cca tgt 112
 303 Met Phe Thr Val Leu Thr Arg Gln Pro Cys
 304 1 5 10
 306 gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc 160
 307 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
 308 15 20 25
 310 ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc 208
 311 Leu Val Val Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
 312 30 35 40
 314 atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt 256
 315 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
 316 45 50 55
 318 att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa 304
 319 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
 320 60 65 70
 322 tgg cca gca gaa aaa gag aat aat acc gga gtc gtc agt caa acc ttc 352
 323 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
 324 75 80 85 90
 326 aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc 400
 327 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
 328 95 100 105
 330 caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg 448
 331 Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
 332 110 115 120
 334 cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc 496
 335 Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
 336 125 130 135
 338 acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat 544
 339 Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
 340 140 145 150
 342 gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac 592
 343 Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
 344 155 160 165 170
 346 ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga 640
 347 Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly
 348 175 180 185
 350 tgg att aca gcc aac tat tta atg gga aat ttc ctg gag aag aac ctg 688
 351 Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu
 352 190 195 200
 354 tgg cac atg tgg gtg cac ccg cat gga gtg gaa acc acg ggt gcc ctg 736

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